

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/573,909
Source: PCT
Date Processed by STIC: 04/07/2006

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/07/2006

PATENT APPLICATION: US/10/573,909

TIME: 14:56:36

Input Set : A:\9237.10WO.ST25.txt

Output Set: N:\CRF4\04072006\J573909.raw

3 <110> APPLICANT: University of Texas Health Science Center at San Antonio
 4 Baseman, Joel
 5 Kannan, Thirumalai
 7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MYCOPLASMA PNEUMONIAE EXOTOXINS
 9 <130> FILE REFERENCE: 9237.10WO
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/573,909
 C--> 11 <141> CURRENT FILING DATE: 2006-03-29
 11 <150> PRIOR APPLICATION NUMBER: US 60/508,607
 12 <151> PRIOR FILING DATE: 2003-10-03
 14 <160> NUMBER OF SEQ ID NOS: 76
 16 <170> SOFTWARE: PatentIn version 3.2
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 591
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Mycoplasma pneumoniae
 23 <400> SEQUENCE: 1
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 26 1 5 10 15
 29 Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
 30 20 25 30
 33 Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
 34 35 40 45
 37 Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
 38 50 55 60
 41 Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
 42 65 70 75 80
 45 Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
 46 85 90 95
 49 Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
 50 100 105 110
 53 Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
 54 115 120 125
 57 Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
 58 130 135 140
 61 Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
 62 145 150 155 160
 65 His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
 66 165 170 175
 69 Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
 70 180 185 190
 73 Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
 74 195 200 205
 77 Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala

CP9-6)

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78      210      215      220
81 Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
82 225      230      235      240
85 Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
86      245      250      255
89 Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
90      260      265      270
93 Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
94      275      280      285
97 Gln Ala Asp Pro Gln Asn Asn Val Phe Leu Val Glu Val Asn Pro
98      290      295      300
101 Lys Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
102 305      310      315      320
105 Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
106      325      330      335
109 Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
110      340      345      350
113 Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
114      355      360      365
117 Gln Asp Ile Ala Ile Ile Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
118      370      375      380
121 Gln Thr Glu Asn Gly Leu Phe Trp Asn Thr Lys Ser Gly Gly Ser Gln
122 385      390      395      400
125 His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
126      405      410      415
129 Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
130      420      425      430
133 Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
134      435      440      445
137 Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
138      450      455      460
141 Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
142 465      470      475      480
145 Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
146      485      490      495
149 Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
150      500      505      510
153 Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
154      515      520      525
157 Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
158      530      535      540
161 His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
162 545      550      555      560
165 Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
166      565      570      575
169 Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
170      580      585      590
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 591

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175 <212> TYPE: PRT

176 <213> ORGANISM: Mycoplasma pneumoniae

178 <400> SEQUENCE: 2

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181 1 5 10 15
184 Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
185 20 25 30
188 Phe Phe Glu His Ile Pro Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
189 35 40 45
192 Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
193 50 55 60
196 Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
197 65 70 75 80
200 Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
201 85 90 95
204 Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
205 100 105 110
208 Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
209 115 120 125
212 Tyr Gln Arg Glu Trp Phe Ile Asp Gly Pro Ile Ala Ala Ala Asn Val
213 130 135 140
216 Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
217 145 150 155 160
220 His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
221 165 170 175
224 Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
225 180 185 190
228 Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
229 195 200 205
232 Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
233 210 215 220
236 Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
237 225 230 235 240
240 Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
241 245 250 255
244 Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
245 260 265 270
248 Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
249 275 280 285
252 Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
253 290 295 300
256 Lys Gln Lys Ser Pro Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
257 305 310 315 320
260 Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
261 325 330 335
264 Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
265 340 345 350
268 Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
269 355 360 365

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272 Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
273      370      375      380
276 Gln Thr Glu Asn Gly Leu Ser Trp Asn Thr Lys Ser Gly Gly Ser Gln
277 385      390      395      400
280 His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
281      405      410      415
284 Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
285      420      425      430
288 Thr Met Arg Ala Ala Ser Thr Phe Val Asp Val Gln Leu Gly Trp
289      435      440      445
292 Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
293      450      455      460
296 Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
297 465      470      475      480
300 Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
301      485      490      495
304 Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
305      500      505      510
308 Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
309      515      520      525
312 Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
313      530      535      540
316 His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
317 545      550      555      560
320 Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
321      565      570      575
324 Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
325      580      585      590
328 <210> SEQ ID NO: 3
329 <211> LENGTH: 591
330 <212> TYPE: PRT
331 <213> ORGANISM: Mycoplasma pneumoniae
333 <400> SEQUENCE: 3
335 Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
336 1      5      10      15
339 Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
340      20      25      30
343 Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
344      35      40      45
347 Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
348      50      55      60
351 Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
352 65      70      75      80
355 Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
356      85      90      95
359 Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
360      100      105      110
363 Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
364      115      120      125

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367 Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
368      130      135      140
371 Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
372 145      150      155      160
375 His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
376      165      170      175
379 Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
380      180      185      190
383 Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
384      195      200      205
387 Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
388      210      215      220
391 Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
392 225      230      235      240
395 Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
396      245      250      255
399 Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
400      260      265      270
403 Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
404      275      280      285
407 Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
408      290      295      300
411 Lys Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
412 305      310      315      320
415 Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
416      325      330      335
419 Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
420      340      345      350
423 Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
424      355      360      365
427 Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
428      370      375      380
431 Gln Thr Glu Asn Gly Leu Phe Trp Asn Thr Lys Ser Gly Gly Ser Gln
432 385      390      395      400
435 His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
436      405      410      415
439 Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
440      420      425      430
443 Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
444      435      440      445
447 Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
448      450      455      460
451 Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
452 465      470      475      480
455 Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
456      485      490      495
459 Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
460      500      505      510
463 Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:76; N Pos. 6,12,15,18,24,30,33,39,42,45,48,69,75,78,81,84,90,93,114
 Seq#:76; N Pos. 117,120,129,132,135,147,150,153,159,162,165,168,171,177,186
 Seq#:76; N Pos. 189,195,198,207,210,219,222,225,228,234,246,249,270,273,276
 Seq#:76; N Pos. 279,282,291,294,300,306,312,318,321,330,333,339,348,357,363
 Seq#:76; N Pos. 366,369,372,375,378,384,393,405,411,414,420,423,426,432,435
 Seq#:76; N Pos. 438,441,447,450,456,459,462,465,471,474,480,489,492,495,498
 Seq#:76; N Pos. 501,504,510,513,516,528,543,558,564,570,582,588,591,594,597
 Seq#:76; N Pos. 600,606,609,612,615,621,624,630,636,639,642,645,648,654,657
 Seq#:76; N Pos. 663,666,669,672,675,678,681,687,693,702,705,708,711,714,720
 Seq#:76; N Pos. 729,732,735,747,771,777,780,783,792,795,798,801,810,819,822
 Seq#:76; N Pos. 825,831,834,837,846,855,864,870,876,891,897,900,906,912,924
 Seq#:76; N Pos. 927,933,939,957,966,975,984,987,990,993,1002,1005,1008,1011
 Seq#:76; N Pos. 1014,1017,1023,1026,1035,1038,1044,1050,1056,1059,1062,1065
 Seq#:76; N Pos. 1068,1071,1077,1080,1101,1104,1113,1116,1122,1131,1134,1137
 Seq#:76; N Pos. 1140,1146,1149,1152,1158,1167,1170,1173,1176,1182,1188,1191
 Seq#:76; N Pos. 1194,1197,1209,1215,1221,1224,1233,1236,1239,1245,1254,1266
 Seq#:76; N Pos. 1278,1281,1287,1296,1299,1305,1308,1311,1314,1317,1326,1332
 Seq#:76; N Pos. 1338,1341,1353,1356,1368,1371,1377,1380,1383,1389,1404,1407
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 Seq#:76; N Pos. 1536,1587,1590,1599,1602,1608,1611,1614,1620,1623,1632,1641
 Seq#:76; N Pos. 1650,1665,1671,1680,1683,1686,1689,1695,1698,1707,1710,1722
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
 per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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 Seq#:36,38,40,41,43,45,46,48,50,52,54,55,57,59,60,62,64,65,66,67,68,72,73,74
 Seq#:75,76

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:0
L:3788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:60
L:3790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:120
L:3792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:180
L:3794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:240
L:3796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:300
L:3798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:360
L:3800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:420
L:3802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:480
L:3804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:540
L:3806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:600
L:3808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:660
L:3810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:720
L:3812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:780
L:3814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:840
L:3816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:900
L:3818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:960
L:3820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1020
L:3822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1080
L:3824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1140
L:3826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1200
L:3828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1260
L:3830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1320
L:3832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1380
L:3834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1440
L:3836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1500
L:3838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1560
L:3840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1620
L:3842 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1680
L:3844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:1740